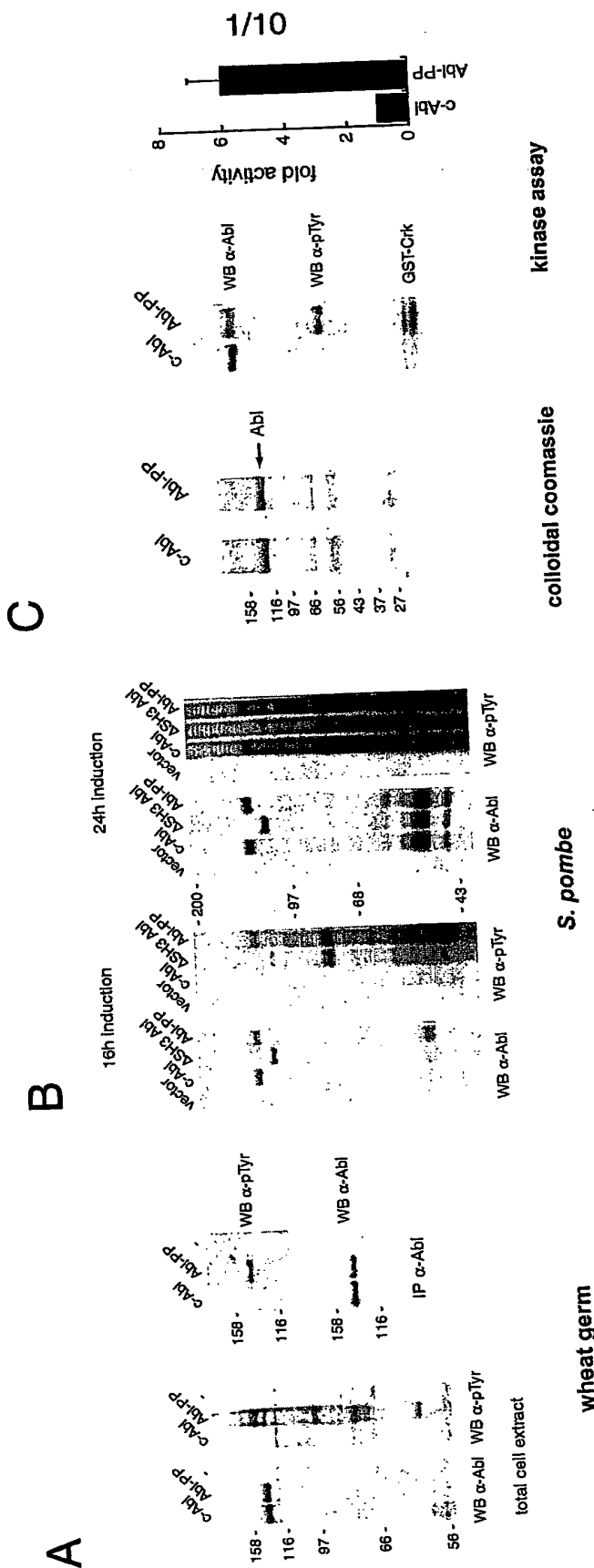


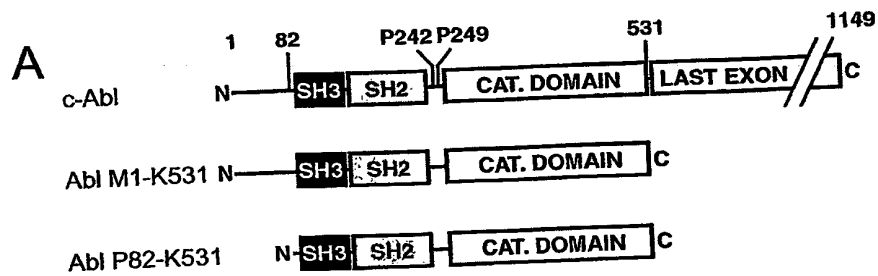
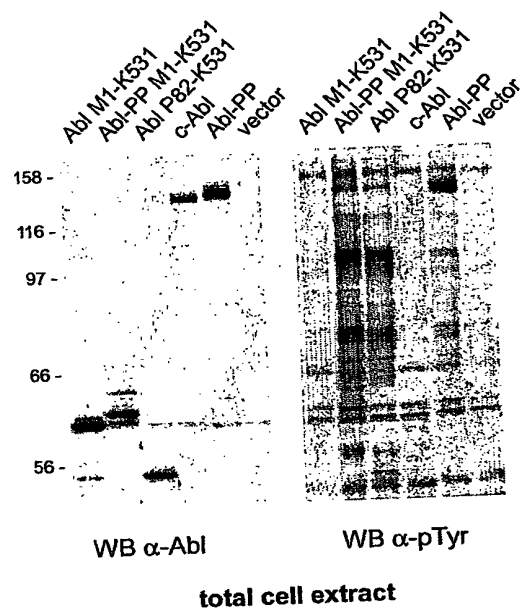
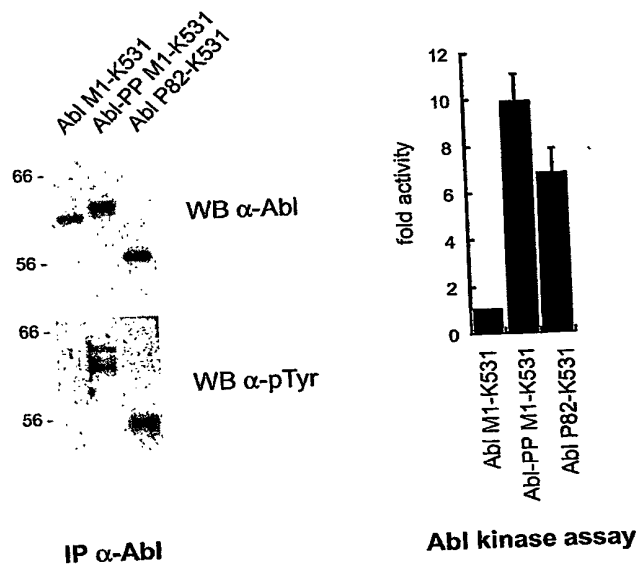
FIG. 1



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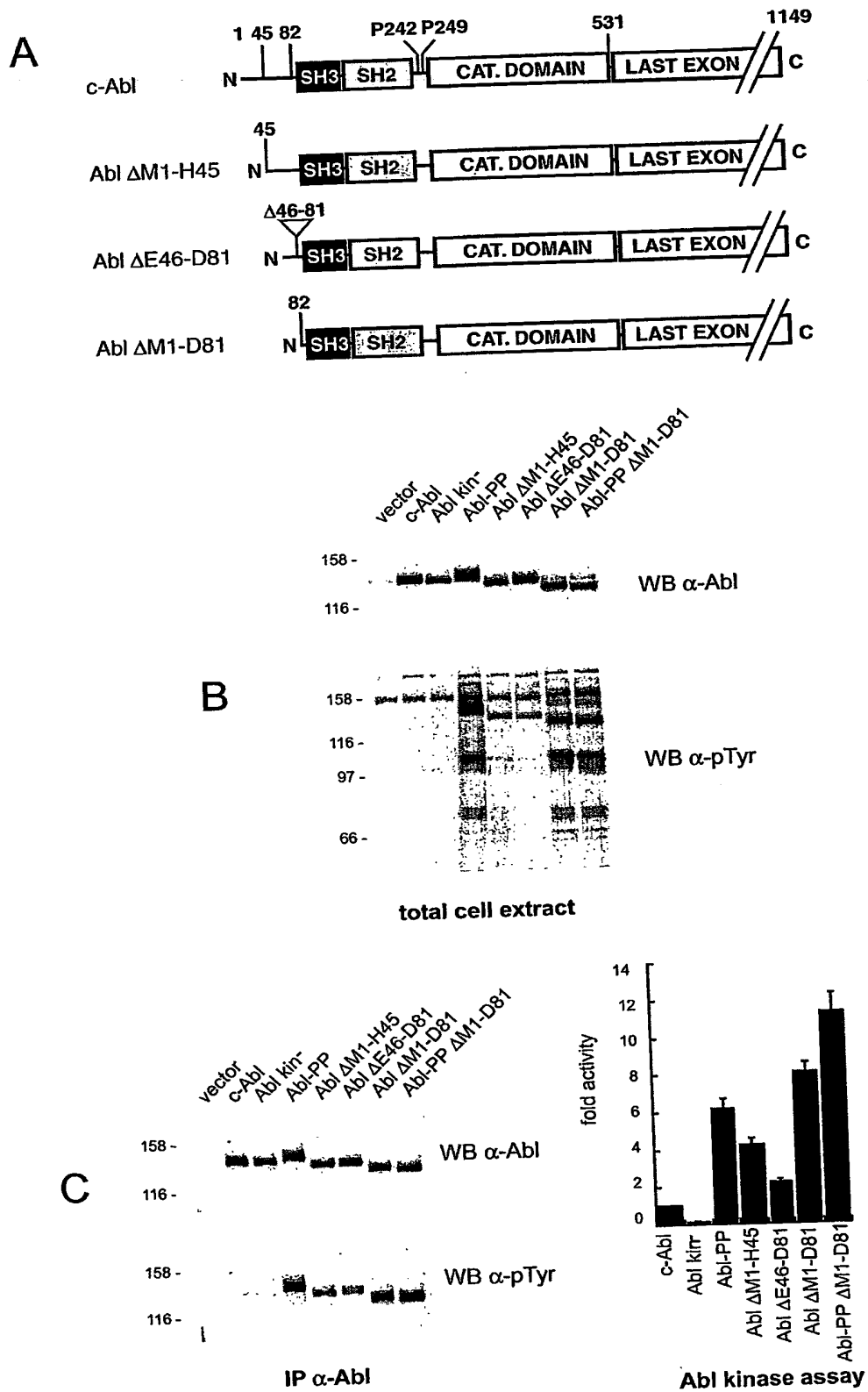
FIG. 2

**B****C**

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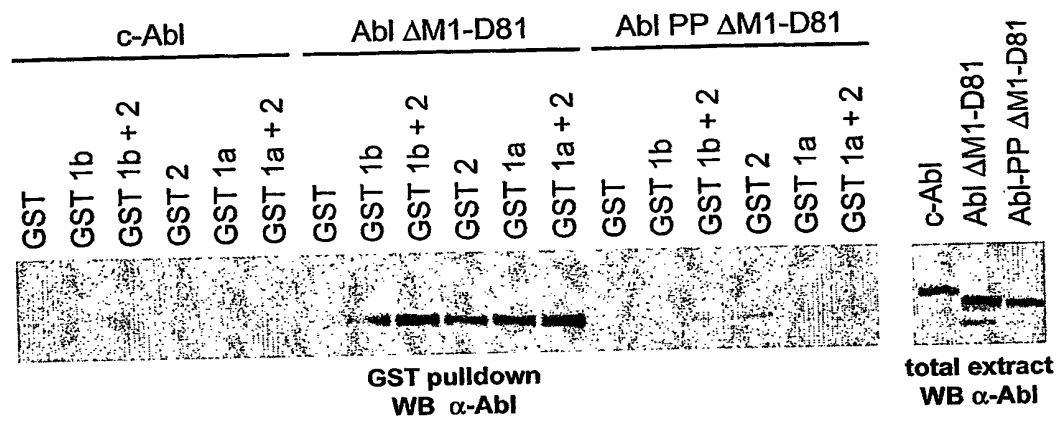
FIG. 3



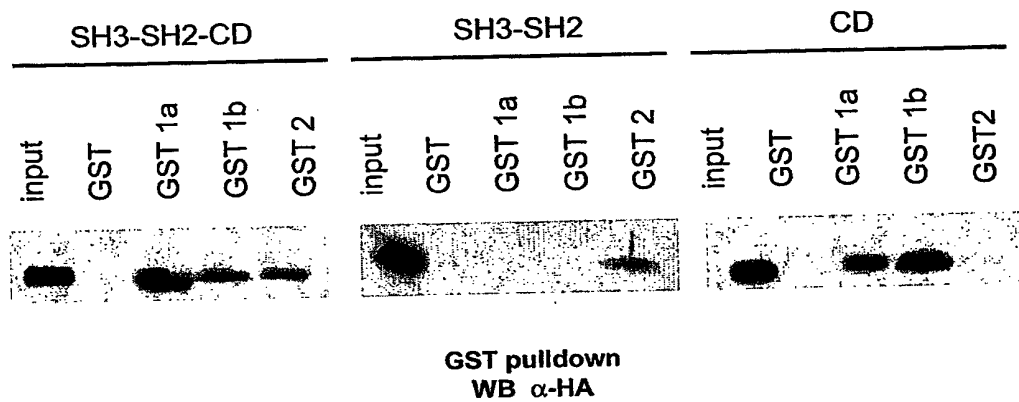
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FIG. 4

A



B



B

IP α -Abl

WB α -pTyr

WB α -Abl

c-Abl
cap 1
cap 2
cap 3
cap 4
cap 5
cap 6
E117K
Abl PP
Vector

Fold activity

Abl kinase assay

cap 1
cap 2
cap 3
cap 4
cap 5
cap 6
E117K
Abl PP
c-Abl

SH3-SH2-CD

CD

input
GST
GST 1b
GST 1b cap 1
GST 2
GST 2 cap 6

input
GST
GST 1b
GST 1b cap 1
GST 2
GST 2 cap 6

GST pulldown
WB α -HA

Detailed description of Panel B: The panel contains four main components. 1. A bar graph titled 'Abl kinase assay' showing 'Fold activity' on the y-axis (0 to 6) for various constructs: c-Abl (1.0), cap 1 (~4.2), cap 2 (~1.8), cap 3 (~1.5), cap 4 (~1.2), cap 5 (~1.5), cap 6 (~3.8), E117K (~2.5), and Abl PP (~5.5). Error bars are shown for each. 2. A Western blot titled 'IP α-Abl' showing bands for c-Abl, cap 1-6, E117K, Abl PP, and Vector. 3. A Western blot titled 'WB α-pTyr' showing bands for the same constructs. 4. A GST pull-down assay at the bottom with two rows of blots. The first row is labeled 'SH3-SH2-CD' and the second 'CD'. Each row has six lanes: 'input', 'GST', 'GST 1b', 'GST 1b cap 1', 'GST 2', and 'GST 2 cap 6'. The 'input' lane shows a strong band. The 'GST' lane shows a weak band. The 'GST 1b' and 'GST 1b cap 1' lanes show strong bands. The 'GST 2' and 'GST 2 cap 6' lanes show very faint bands.

Construct	Fold activity
c-Abl	1.0
cap 1	~4.2
cap 2	~1.8
cap 3	~1.5
cap 4	~1.2
cap 5	~1.5
cap 6	~3.8
E117K	~2.5
Abl PP	~5.5

A

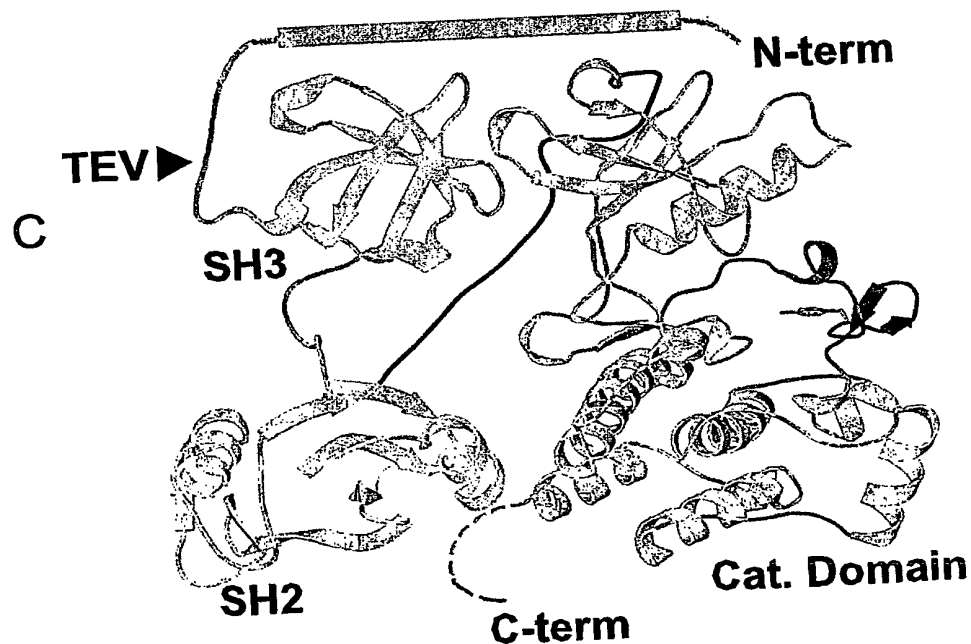
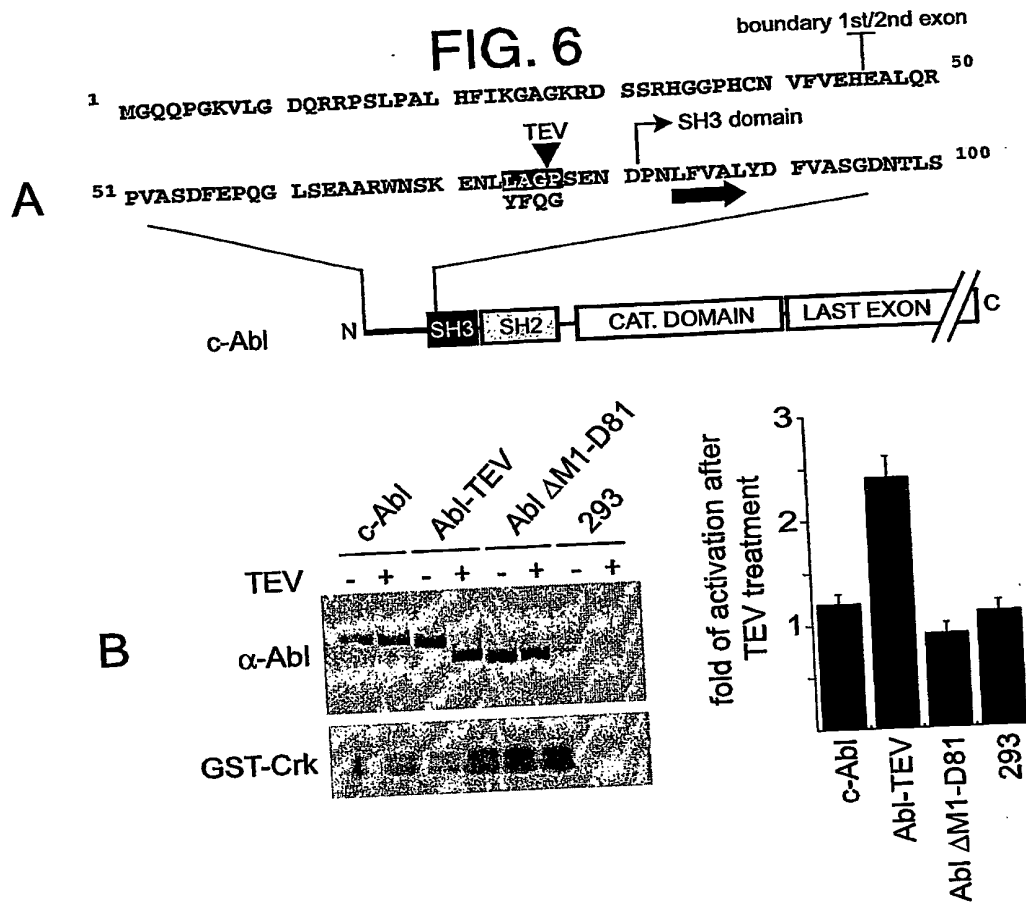
boundary 1st/2nd exon

cap 1 cap 2 cap 3 cap 4 cap 5 cap 6

Ab1 1b 1¹MGQPGKVLGDQRRPSLPALHFIKGAGKRDSSRHGPHCNVFEHEALQRPVADFEFQGLSEAARWNSKENLLAGPSEN⁸⁰

Ab1 1a 1¹MEICLKLVGCKSK-----KGLS---SS-----SSCYLEEALQRPVADFEFQGLSEAARWNSKENLLAGPSEN⁶¹

FIG. 6



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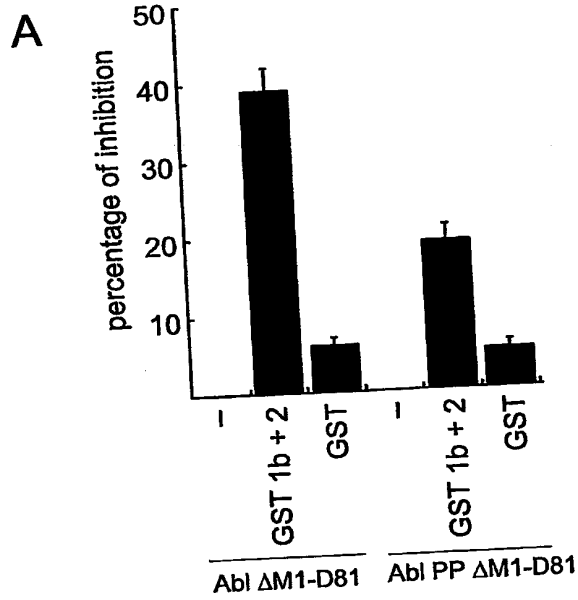


FIG. 7

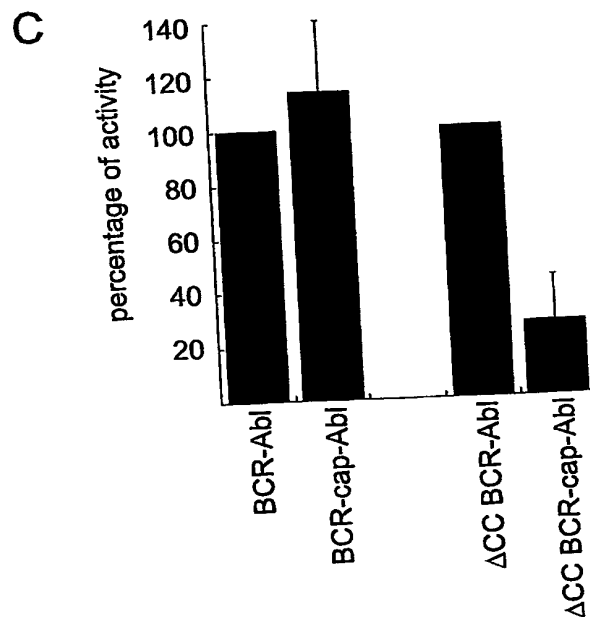
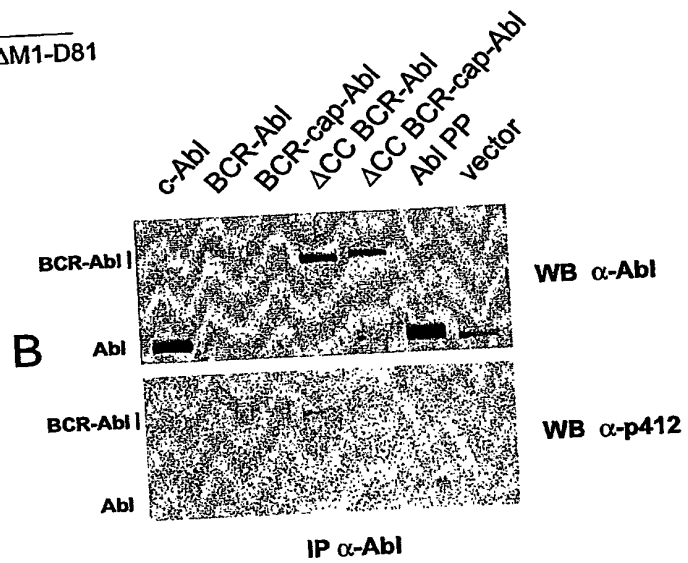


FIG 8

hAbl1a MLEICLKL-----VGCKSK-----KGLSSSSS-----C-YLEE-
 mAb1I MLEICLKL-----VGCKSK-----KGLSSSSS-----C-YLEEH
 hAbl1b MGQQPGKV-----LGDQRRPSLPALHFIKGAGKRDSSRHGGP-----HCNVFVEH
 mAb1IV MGQQPGKV-----LGDQRRPSLPALHFIKGAGKRDSSRHGGP-----HCNVFVEH
 hArg1a --MVLGTV-----LLPPN-----TYGRDQDTS-----LCCLCTEA
 hArg1b MGQQVGRVGEAPGLQQPQPRGIRGSSAARPSGRRRDPAGRTTETGFNIFTQHDHFASCVED

 hAbl1a -----ALQRPVASFEPQGL***SEAARWNSKENLL***LAGPSEN----- 61
 mAb1I -----EALQRPVASFEPQGL***SEAARWNSKENLL***LAGPSEN----- 63
 hAbl1b -----EALQRPVASFEPQGL***SEAARWNSKENLL***LAGPSENDPNLFVALYDFV 92
 mAb1IV -----EALQRPVASFEPQGL***SEAARWNSKENLL***LAGPSEN----- 80
 hArg1a ---SESALPDLTEALHRPYGCDVEPQAL***NEAIRWSSKENLL***GATES----- 71
 hArg1b GFEGDKTGGSSPEALHRPYGCDVEPQAL***NEAIRWSSKENLL***GATES----- 107

Legend:

Bold: cap 1 domain

Underlined: cap 6 domain

Bold italic: conserved domain upstream of cap 6 domain that forms an alpha helix with cap 6 domain

FIG 9

hAb11a -----
mAb1I -----
hAb11b -----
mAb1IV -----
hArg ATGGGGCAGCAGGTGGGCCGCGTCGGGGAAGCTCCGGGGCTCCAGCAGCCTCAGCCCCGC 60

hAb11a -----
mAb1I -----
hAb11b -----ATGGGGCAGCAGCCTGGAAAAGTTCTTGGGGACCAAAG 38
mAb1IV -----ATGGGGCAGCAGCCTGGAAAAGTTCTTGGGGACCAAAG 38
hArg GGGATCCGGGGCAGCAGTGCAGCCAGGCCCTCCGGCCGAGGCGGGACCCGGCGGGGCGC 120

hAb11a -----ATGTTGGAGATCTGCCTGAAGCTGGTGGGCTGCAAATCCAAGAAGG 46
mAb1I -----ATGTTGGAGATCTGTTTGAAGTTGGTGGGCTGCAAATCCAAGAAGG 46
hAb11b AAGGCCTAGTTTGCCCGCCCTGCATTTTATCAAAGGGGCAGGGAAGAGGGACTCATCGAG 98
mAb1IV AAGGCCTAGTTTGCCCGCCCTGCATTTTATCAAAGGGGCAGGGAAGAGGGACTCATCGAG 98
hArg ACCACAGAGACCGGCTTCAATATCTTCACCCAGCATGATCACTTTGCCAG-CTGTGTGGA 179

hAb11a GGCTGTCCTCGTCCTCCAGCTGTTATCTGGAAGAA-----GCCCTGCAGAGGCCAGT 98
mAb1I GGCTCTCTTCGTCCTCCAGCTGCTACCTGGAGGAACAC--GAAGCCCTGCAGAGGCCAGT 104
hAb11b GCATGGGGGC-CCACACTGCAATGTCTTTGTGGAACAC--GAAGCCCTGCAGAGGCCAGT 155
mAb1IV GCATGGGGGC-CCACACTGCAATGTCTTTGTGGAACAC--GAAGCCCTGCAGAGGCCAGT 155
hArg GGATGGATTTGAGGGAGACAAGACTGGAGGCAGTAGTCCAGAAGCTTTGCATCGTCCCTA 239

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hAb11a GGCATCTGACTTTGAGCCCCAGGGTCTCAGCGAAGCAGCTCGATGGAACTCCAAGGAAAA 158
mAb1I GGCATCTGACTTTGAGCCCCAGGGTCTCAGCGAAGCAGCTCGATGGAACTCCAAGGAAAA 164
hAb11b GGCATCTGACTTTGAGCCCCAGGGTCTCAGCGAAGCAGCTCGATGGAACTCCAAGGAAAA 215
mAb1IV GGCATCTGACTTTGAGCCCCAGGGTCTCAGCGAAGCAGCTCGATGGAACTCCAAGGAAAA 215
hArg TGGTTGTGATGTTGAACCCAGGCACTAAATGAGGCTATCAGGTGGAGCTCCAAGGAGAA 299

hAb11a CCTTCTTGCTGGGCCCAGTGAAAAAT----- 183
mAb1I CCTTCTTGCTGGGCCCAGTGAAAAAT----- 189
hAb11b CCTTCTTGCTGGGCCCAGTGAAAAATGACCCCAACCTTTTTGTGGCACTCTATGATTTTGT 275
mAb1IV CCTTCTTGCTGGGCCCAGTGAAAAAT----- 240
hArg CTTGCTCG---GAGCCACTGAGAGTGACCCTAAT----- 330

hAb11a -

mAb1I -

hAb11b G 276

mAb1IV -

hArg -